

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/889,314

CRF Processing Date: 1/17/2002 #5
 Edited by:
 Verified by: (STIC staff)

ENTERED

P4/09
 1/17/2002 #5
 BC

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "garbage" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

☐ Deleted extra, invalid, headings used by an applicant, specifically:

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☒ Other:

Corrected C1407, C1417, C1507, C1517 sections

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/889,314

DATE: 01/17/2002

TIME: 08:04:08

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01172002\I889314.raw

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3 <110> APPLICANT: BURNIE, JAMES PETER
4   MATTHEWS, RUTH CHRISTINE
6 <120> TITLE OF INVENTION: MEDICAMENT
8 <130> FILE REFERENCE: 050885-0281578
10 <140> CURRENT APPLICATION NUMBER: 09/889,314
11 <141> CURRENT FILING DATE: 2001-07-16
13 <150> PRIOR APPLICATION NUMBER: GB 9902555.3
14 <151> PRIOR FILING DATE: 1999-02-05
16 <150> PRIOR APPLICATION NUMBER: PCT/GB00/00237
17 <151> PRIOR FILING DATE: 2000-01-28
20 <160> NUMBER OF SEQ ID NOS: 16
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1491
26 <212> TYPE: DNA
27 <213> ORGANISM: Chlamydia pneumoniae
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(1491)
33 <400> SEQUENCE: 1
34 gat aca aac atg tct att tca tct tct tca gga cct gac aat caa aaa   48
35 Asp Thr Asn Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys
36   1           5           10           15
38 aat atc atg tct caa gtt ctg aca tcg aca ccc cag ggc gtg ccc caa   96
39 Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln
40           20           25           30
42 caa gat aag ctg tct ggc aac gaa acg aag caa ata cag caa aca cgt   144
43 Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg
44           35           40           45
46 cag ggt aaa aac act gag atg gaa agc gat gcc act att gct ggt gct   192
47 Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala
48           50           55           60
50 tct gga aaa gac aaa act tcc tcg act aca aaa aca gaa aca gct cca   240
51 Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro
52 65           70           75           80
54 caa cag gga gtt gct gct ggg aaa gaa tcc tca gaa agt caa aag gca   288
55 Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala
56           85           90           95
58 ggt gct gat act gga gta tca gga gcg gct gct act aca gca tca aat   336
59 Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn
60           100          105          110
62 act gca aca aaa att gct atg cag acc tct att gaa gag gcg agc aaa   384
63 Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys
64           115          120          125
66 agt atg gag tct acc tta gag tca ctt caa agc ctc agt gcc gcg caa   432
67 Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln
68           130          135          140

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70 atg aaa gaa gtc gaa gcg gtt gtt gtt gct gcc ctc tca ggg aaa agt 480
71 Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser
72 145 150 155 160
74 tcg ggt tcc gca aaa ttg gaa aca cct gag ctc ccc aag ccc ggg gtg 528
75 Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val
76 165 170 175
78 aca cca aga tca gag gtt atc gaa atc gga ctc gcg ctt gct aaa gca 576
79 Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala
80 180 185 190
82 att cag aca ttg gga gaa gcc aca aaa tct gcc tta tct aac tat gca 624
83 Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala
84 195 200 205
86 agt aca caa gca caa gca gac caa aca aat aaa cta ggt cta gaa aag 672
87 Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys
88 210 215 220
90 caa gcg ata aaa atc gat aaa gaa cga gaa gaa tac caa gag atg aag 720
91 Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys
92 225 230 235 240
94 gct gcc gaa cag aag tct aaa gat ctc gaa gga aca atg gat act gtc 768
95 Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val
96 245 250 255
98 aat act gtg atg atc gcg gtt tct gtt gcc att aca gtt att tct att 816
99 Asn Thr Val Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile
100 260 265 270
102 gtt gct gct att ttt aca tgc gga gct gga ctc gct gga ctc gct gcg 864
103 Val Ala Ala Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala
104 275 280 285
106 gga gct gct gta ggt gca gcg gca gct gga ggt gca gca gga gct gct 912
107 Gly Ala Ala Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala
108 290 295 300
110 gcc gca acc acg gta gca aca caa att aca gtt caa gct gtt gtc caa 960
111 Ala Ala Thr Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln
112 305 310 315 320
114 gcg gtg aaa caa gct gtt atc aca gct gtc aga caa gcg atc acc gcg 1008
115 Ala Val Lys Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala
116 325 330 335
118 gct ata aaa gcg gct gtc aaa tct gga ata aaa gca ttt atc aaa act 1056
119 Ala Ile Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr
120 340 345 350
122 tta gtc aaa gcg att gcc aaa gcc att tct aaa gga atc tct aag gtt 1104
123 Leu Val Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val
124 355 360 365
126 ttc gct aag gga act caa atg att gcg aag aac ttc ccc aag ctc tcg 1152
127 Phe Ala Lys Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser
128 370 375 380
130 aaa gtc atc tcg tct ctt acc agt aaa tgg gtc acg gtt ggg gtt ggg 1200
131 Lys Val Ile Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly
132 385 390 395 400
134 gtt gta gtt gcg gcg cct gct ctc ggt aaa ggg att atg caa atg cag 1248

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135 Val Val Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln
136          405          410          415
138 ctc tcg gag atg caa caa aac gtc gct caa ttt cag aaa gaa gtc gga 1296
139 Leu Ser Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly
140          420          425          430
142 aaa ctg cag gct gcg gct gat atg att tct atg ttc act caa ttt tgg 1344
143 Lys Leu Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp
144          435          440          445
146 caa cag gca agt aaa att gcc tca aaa caa aca ggc gag tct aat gaa 1392
147 Gln Gln Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu
148          450          455          460
150 atg act caa aaa gct acc aag ctg ggc gct caa atc ctt aaa gcg tat 1440
151 Met Thr Gln Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr
152 465          470          475          480
154 gcc gca atc agc gga gcc atc gct ggc gca cat aaa acc aat aat ttt 1488
155 Ala Ala Ile Ser Gly Ala Ile Ala Gly Ala His Lys Thr Asn Asn Phe
156          485          490          495
158 taa 1491
162 <210> SEQ ID NO: 2
163 <211> LENGTH: 496
164 <212> TYPE: PRT
165 <213> ORGANISM: Chlamydia pneumoniae
167 <400> SEQUENCE: 2
168 Asp Thr Asn Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys
169 1 5 10 15
171 Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln
172 20 25 30
174 Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg
175 35 40 45
177 Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala
178 50 55 60
180 Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro
181 65 70 75 80
183 Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala
184 85 90 95
186 Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn
187 100 105 110
189 Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys
190 115 120 125
192 Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln
193 130 135 140
195 Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser
196 145 150 155 160
198 Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val
199 165 170 175
201 Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala
202 180 185 190
204 Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala
205 195 200 205

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```

207 Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys
208      210      215      220
210 Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys
211 225      230      235      240
213 Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val
214      245      250      255
216 Asn Thr Val Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile
217      260      265      270
219 Val Ala Ala Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala
220      275      280      285
222 Gly Ala Ala Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala
223      290      295      300
225 Ala Ala Thr Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln
226 305      310      315      320
228 Ala Val Lys Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala
229      325      330      335
231 Ala Ile Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr
232      340      345      350
234 Leu Val Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val
235      355      360      365
237 Phe Ala Lys Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser
238      370      375      380
240 Lys Val Ile Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly
241 385      390      395      400
243 Val Val Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln
244      405      410      415
246 Leu Ser Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly
247      420      425      430
249 Lys Leu Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp
250      435      440      445
252 Gln Gln Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu
253      450      455      460
255 Met Thr Gln Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr
256 465      470      475      480
258 Ala Ala Ile Ser Gly Ala Ile Ala Gly Ala His Lys Thr Asn Asn Phe
259      485      490      495

```

262 <210> SEQ ID NO: 3

263 <211> LENGTH: 302

264 <212> TYPE: PRT

265 <213> ORGANISM: Artificial Sequence

267 <220> FEATURE:

268 <223> OTHER INFORMATION: Description of Artificial Sequence: Codon

269 optimised N-terminal section of Chlamydia

270 pneumoniae protein

272 <220> FEATURE:

273 <221> NAME/KEY: UNSURE

274 <222> LOCATION: (1)..(30)

275 <223> OTHER INFORMATION: S-tag and thrombin cleavage site

277 <220> FEATURE:

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278 <223> OTHER INFORMATION: Positions (297)..(302) comprise Histidine tag

280 <400> SEQUENCE: 3

281 Met Lys Glu Thr Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser

282 1 5 10 15

284 Pro Asp Leu Gly Thr Leu Val Pro Arg Gly Ser Ala Ile Ser Asp Pro

285 20 25 30

287 Asp Thr Asn Met Ser Ile Ser Ser Ser Gly Pro Asp Asn Gln Lys

288 35 40 45

290 Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln

291 50 55 60

293 Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg

294 65 70 75 80

296 Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala

297 85 90 95

299 Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro

300 100 105 110

302 Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala

303 115 120 125

305 Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn

306 130 135 140

308 Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys

309 145 150 155 160

311 Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln

312 165 170 175

314 Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser

315 180 185 190

317 Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val

318 195 200 205

320 Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala

321 210 215 220

323 Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala

324 225 230 235 240

326 Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys

327 245 250 255

329 Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys

330 260 265 270

332 Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val

333 275 280 285

335 Asn Thr Val Ala Ala Ala Leu Glu His His His His His His

336 290 295 300

339 <210> SEQ ID NO: 4

340 <211> LENGTH: 9

341 <212> TYPE: PRT

342 <213> ORGANISM: Chlamydia pneumoniae

344 <400> SEQUENCE: 4

345 Ser Ala Lys Leu Glu Thr Pro Glu Leu

346 1 5

349 <210> SEQ ID NO: 5

350 <211> LENGTH: 7

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/889,314

DATE: 01/17/2002

TIME: 08:04:09

Input Set : A:\PTO.AMC.txt

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